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On nucleic acid search, using sw model.

Run on: April 2, 2002, 20:21:08 : Search time 160.55 Seconds

Title: US-09-486-094-1

Perfect score: 10

Sequence: aggccgtggatggatggatgat.....gaaatcgatcggatccgg 110

Scoring table: IDENTITY_NUC

GapPen 10.0 , Gapext 1.0

Searched: 9/05/21 seqs: 42866569 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Maximum Match 10%

List length: 45 summaries

Maximum Match 10%

Database : SIBSDB

Scoring: Scopula/geneid/geneseed/geneseed/NAI980.DAT*

1: /SIBSDB/geneid/geneseed/geneseed/NAI981.DAT*

2: /SIBSDB/geneid/geneseed/geneseed/NAI982.DAT*

3: /SIBSDB/geneid/geneseed/geneseed/NAI983.DAT*

4: /SIBSDB/geneid/geneseed/geneseed/NAI984.DAT*

5: /SIBSDB/geneid/geneseed/geneseed/NAI985.DAT*

6: /SIBSDB/geneid/geneseed/geneseed/NAI986.DAT*

7: /SIBSDB/geneid/geneseed/geneseed/NAI987.DAT*

8: /SIBSDB/geneid/geneseed/geneseed/NAI988.DAT*

9: /SIBSDB/geneid/geneseed/geneseed/NAI989.DAT*

10: /SIBSDB/geneid/geneseed/geneseed/NAI990.DAT*

11: /SIBSDB/geneid/geneseed/geneseed/NAI991.DAT*

12: /SIBSDB/geneid/geneseed/geneseed/NAI992.DAT*

13: /SIBSDB/geneid/geneseed/geneseed/NAI993.DAT*

14: /SIBSDB/geneid/geneseed/geneseed/NAI994.DAT*

15: /SIBSDB/geneid/geneseed/geneseed/NAI995.DAT*

16: /SIBSDB/geneid/geneseed/geneseed/NAI996.DAT*

17: /SIBSDB/geneid/geneseed/geneseed/NAI997.DAT*

18: /SIBSDB/geneid/geneseed/geneseed/NAI998.DAT*

19: /SIBSDB/geneid/geneseed/geneseed/NAI999.DAT*

20: /SIBSDB/geneid/geneseed/geneseed/NA2000.DAT*

21: /SIBSDB/geneid/geneseed/geneseed/NA2001.DAT*

22: /SIBSDB/geneid/geneseed/geneseed/NA2002.DAT*

Prod. No.: 1

No. is the number of results predicted by chance to have a P-value less than or equal to 0.05 and is derived by analysis of the total score distribution.

C	12	27.4	24.9	5362	18	ANP97296
C	13	27.4	24.9	5362	18	ANP97294
C	14	27.7	24.7	5362	18	ANP97292
C	15	27.7	24.7	5362	18	ANP97291
C	16	27.7	24.7	5393	22	ANP97558
C	17	27.2	24.7	405	22	AN116244
C	18	27.2	24.7	405	22	AN11835
C	19	26.8	24.5	6516	22	ANC75901
C	20	26.8	24.5	1920	22	ANH45250
C	21	26.8	24.4	1920	22	ANH45250
C	22	26.4	24.0	4650	22	ANH7670
C	23	26.2	23.8	758	22	ANH95445
C	24	26.2	23.8	1572	22	ANB10094
C	25	26.2	23.8	2207	22	ANB10097
C	26	26.2	23.3	5003	22	ANB10097
C	27	26.2	23.3	3072	21	ANB10097
C	28	26	23.6	301	21	ANH0779
C	29	26	23.6	2201	21	ANH14988
C	30	26	23.6	2201	21	ANH14988
C	31	26	23.6	2243	21	ANH14988
C	32	26	23.6	2243	21	ANH14988
C	33	25.6	23.3	170	21	ANQ9015
C	34	25.6	23.3	1331	22	ANB14424
C	35	25.6	23.3	1020	22	ANB14425
C	36	25.6	23.3	5003	22	ANB14425
C	37	25.6	23.3	6481	22	ANL198183
C	38	25.6	23.3	10625	22	ANC1336
C	39	25.4	23.1	318	20	ANX1144
C	40	25.4	23.1	1150	20	ANX1144
C	41	25.4	23.1	1150	20	ANX1144
C	42	25.4	23.1	5714	20	ANX1144
C	43	25	22.9	1083	21	ANAP2728
C	44	25	22.7	662	21	ANAP2728
C	45	25	22.7	2921	22	ANH16003

ALIGNMENTS

RESULT 1
SIBSDB

1

ANX19727

standard DNA; 110 bp.

XX

ANX19727;

ANX19727

AAA99732 standard; DNR: 44 BP .
 AAA99732;
 AAA99732;
 22-JUN-1999 (first entry)
 Olgo #3 loc. scorpion toxin gene.
 Toxin, antroctokinin; bacterium; infection; as;
 resistance; fungus;

Example 1: page 12; 37PP; French.
TC This sequence corresponds to a mitochondrial used to generate a signal peptide sequence linked to the gene encoding the toxin androctoxin.
CC From the scorzonera Androctonus australis, for expression in plants.
CC Transient: Plants containing androctoxin genes are stated to be
CC Cicerchia latifolia, *C. sativa*, *C. arietinum*, *C. chinense*,
CC *Cicer arietinum* or *Phytolacca cinnamomea*.

Thanatiae: fungal disease; bacterial disease; *Cercospora beticula*; *Cladophorum herbarium*; *Fusarium cunorum*; *F. graninearum*; *Phyllosticta cinnamonii*; selection marker; plant transformation; herbicide resistance; PR-1a gene; tobacco; ss.

PR 15-APR-1998 : 98FR-0004933 .
XX DA (RHON) RHOMP - DOUTINIC AGROCHIMI

